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Input file 17867cons; Output File 17867tra
Sequence length 3366

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CCCCCGCTCCGGCATGATTAAAGATTAATTCTATGTATTGAAAATTTGTCAGACCCCCATGTGACATAACTGGAGCCA
80 90 100 110 120 130 140 M F H
GTCAGTCCCATAAGAACATACGAGATTAGCCTGGATATTAACTTGCTCTAGAGAAATAGATTC ATG TTC CAT
146
S S A M V N S H R K P M F N I H R G F Y
TCT TCT GCA ATG GTT ATT CAA CAC AGA AAA CCA ATG TTT AAC ATT CAC AGA GGA TTT TAC
69
TGC TTA ACA GCA ATC TTG CCC CAA ATA TGC ATT TGT TCT CAG TTC TCA GTG CCA TCT AGT
43
TAT CAC TTC ACT GAG GAT CCT GGG GCT TTC CCA GTA GCC ACT ATT GGG GAA CGA TTT CCT
129
TGG CAG GAG CTA AGG CTC CCC AGT GTG GTC ATT CCT CTC CAT ATT GAC CTC TTT GTC CAC
63
P N I T S P S Y V P L H Y D L F Y H
CCC AAT CTC ACC TCT CTG GAC TTT GTT GCA TCT GAG AAG ATC GAA GTC TTG GTC AGC AAT
189
A T Q F F E D P G A F P Y A T N G F R F P
GCT ACC CAG TTT ATC ATC TTG CAC AGC AAA GAT CCT GAA ATC AGC ATT GCC ACC CTT CAG
103
TCA GAG GAA GAT TCA AGA TAC ATG AAA CCA GGA AAA GAA CTG AAA GTT TTG AGT TAC CCT
369
A H E Q I A L V P E K L K V I S Y P
GCT CAT GAA CAA ATT GCA CTG CTG GTT CCA GAG AAA CCT ACG CCT CAC CTG AAA TAC TAT
143
V A M D E Q A K L G D G F F E G G F Y K S T
GTG GCT ATG GAC TTC CAA GCC AAG TTA GGT GAT GGC TTT GAA GGG TTT TAT AAA AGC ACA
549
Y R T L G G E T R T L A V T D F E P T Q
TAC AGA ACT CTT GGT GGT GAA ACA AGA ATT CTT GCA GTA ACA GAT TTT GAG CCA ACC CAG
609
A R M A F E P F D E P L F K A N F S I K
GCA CGC ATG GCT CCT TGC TTT GAT GAA CGG TTG TTC AAA GGC AAC TTT TCA ATC AAC
223
I R R F S R H A L S N M P K V K T I F
ATA CGA AGA GAG AGC AGG CAT ATT GCA CTA TCC AAC ATG CCA AAG GTT AAG ACA ATT GAA
729
L T GAA GGA GGT CTT TTG GAA GAT CAA TTT GAA ACT ACT GTC AAA ATG AGT ACA TAC CTT
243
Y A Y I V F D F H S L S G F T S S G V K
GTA GCC TAC ATA GTT TGT GAT TTC CAC TCT CTG AGT GGC TTC ACT TCA TCA GGG GTC AAG
849
G T G T C C A T C T A T G C A G A A A C C G A A T C A C T A T G T T G C A G G C A T C A
303
L K L D F Y F K Y F D I Y Y P L S K L
CTG AAG CTA CTT GAT TTT TAT GAA AAG TAC TTT GAT ATC TAC TAT CCA CTC TCC AAA CTG
323
D T T A A T T G C T A T T C C G A C T T G C A C T T G C A G G C C A A G C C A C T A T G T
343
GAT TTA ATT GCT ATT CCT GAC TTT GCA CCT GGA GCC ATG GAA ATT TGG GGC CTC ATT ACA
1029
TAT AGG GAG AGC TCA CTG CTT GAT GAC CCC AAG ACC TCT TGT GCT TCC GAT AAA CTG TTG
363
V T R V I A H E L A H Q V F G N L V T M
GTC ACC AGA GTC ATA GCC CAT GAA CTG CGG CAC CAG TGG TTT GGC AAC CTG GTC ACA ATG 1149

FIG. 1A.

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E W V N D I V L K F G F A K Y M E L I A 403
GAA TGG TGG AAT GAT ATT TGG CTT AAC GAG GGT TTT GCA AAA TAC ATG GAA CTT ATC ATC GCT 1208
V N A T Y P E L Q F D D Y F L N V C F E 423
GTT AAT GCT ACA TAT CCA GAG CTG CAA TTT GAT GAC TAT TTT TTG AAT GTG TGT TTT GAA 1269
V T T K D S L N S S R P I S K P A F T P 443
GTA ATT ACA AAA GAT TCA TTG AAT TCA TCC CGC CCT ATC TCC AAA CCA CGG GAA ACC CCG 1329
T Q I M F E M F E P E V S N K G A C I L N 463
ACT CAA ATA CAG GAA ATG TTT GAT GAA GTT TCC TAT AAC AAG GGA GCT TGT ATT TTG AAT 1389
M L K D F L G F E K F Q K G I I D Y L K 483
ATG CTC AAG GAT TTT CTG GGT GAG GAG AAA TTC CAG AAA GGA ATA ATT CAG TAC TTA AAG 1449
K F S Y R N A K N D I V S S L S N S F 503
AAG TTC AGC TAT AGA AAT CCT AAC AGT GAT GAC TTG AGC AGT CTG TCA AAT AGT TGT 1509
I F S D F T S G G V C H S D P K M T S N 523
TTA GAA AGT GAT TTT ACA TCT GGT GGA GTT TGT CAT TCG GAT CCC AAG ATG ACA AGT AAC 1569
M L A F L G F N A E V K F M M T T W T L 543
ATG CTC GCC TTT CTG GGG GAA AAT GCA GAG GTC AAA GAG ATG ATG ACT ACA TGG ACT CTC 1629
Q K G I P L L V V K Q D G C S I R L Q Q 563
CAG AAA GGA ATC CCC CTG CTG GTG GTT AAA CAA CAC GAC GGG TGT TCA CTC CGA CTG CAA CAG 1689
E R F I Q G Y F Q E D P F V R A L Q F R 583
GAG CGC TTC CTC CAG GGG GTT TTC CAG GAA GAC CCT GAA TGG AGG GCC CTG CAG GAG AGG 1749
Y L V H I P I V S T S S S N V I H R H 603
TAC CTG TGG CAT ATC CCA TTG ACC TAC TCC ACC AGT TCT TAT AAC GTG ATC CAC AGA CAC 1809
I L K S K T D T I D L P F K T S V V K F 623
ATT CTA AAA TCA AAG ACA GAT ACT CTG GAT CTA CCT GAA AAG ACC AGT TGG GTG AAA TTT 1869
N V D S N G Y I V H Y F G H G W D Q C 643
AAT GTG GAC TCA AAT GGT TAC TAC ATC GTT CAC TAT GAG GGT CAT GGA TGG GAC CAA CTC 1929
I T Q I N Q N H I T I R P K D R V G L I 689
ATT ACA CAG CTG AAT CAG AAC AAC ACA CTT CTC AGA CCT AAG GAC AGA GTA GGT CTG ATT 1989
H D V F I Q L V G A G R T L D K A I D M 683
CAT GAT GTG TTT CAG CTA GTT GGT GCA GGG AGA CTG ACC CTA GAC AAA GCT CTT GAC ATG 2049
T A C T A C C T C A A C A T G A A A C A G C G C C G C A C T C T G A A G G T C T G A G T A C T G 2103
E S F Y H M M D R R N I S D I S E N I K 723
GAA TCG TTT TAC CAC ATG ATG GAC AGA AGG AAT ATT TCA GAT ATC TCT GAA AAC CTC AAG 2169
P Y I Q Y E K P I D R Q S V S D K G 743
CTG TAC CTT CTT CAG TAT TTT AAC GCA CTG ATT GAC AGG AAC AGC TGG AGT GAC AAC GGC 2229
S V V D R M I R S A I K C I A F D L N H 763
TCA GTC TGG GAC AGG ATG CTC CGC TCG GCT CTC TTG AAG CTG GCC TGT GAC CTG AAC CAT 2289
A P F I Q K A A F L F S Q W M E S S G K 783
GCT CCT TGC ATC CAG AAA GCT GCT GAA CTC TCC TCC CAG TGG ATG GAA TCC AGT GGA AAA 2349
I N I P T D V I K T V Y S V G A Q T T A 803
TTA AAT ATA CCA ACA GAT GTT TTA AAG ATT GTG TAT TCT GTG GGT GCT CAG ACA ACA GCA 2409
G W N Y L I F Q Y F E L S M S S A F Q N K 823
GGA TGG AAT TAC CTT TTA GAG CAA TAT GAA CTG TCA ATG TCA AGT GCT GAA CAA AAC AAA 2469

FIG. 1B.

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A T C T G T A T G C T T T G T C A A C G A G C A A G C A T C A G G A A A G T T A C T G A G T T A A T T G A A C T A 843
G M E G K V I K T P N L A A L L H A I A 863
GGA ATG GAA GGA AAG GTT ATC AAG ACA CAG AAC TTG GCA GCT CTC CTT CAT GCG ATT GCC 2589
R R P K G Q Q L A V D F V R F N W T H L 883
AGA CGT CCA AAG GGG CAG CAA CTA GCA TGG GAT TTT GTA AGA GAA AAT TGG ACC CAT CTT 2649
L K K F D L G S Y D I R M I I S G T T A 903
CTG AAA AAA TTT GAC TTG GGC TCA TAT GAC ATA AGG ATG ATC ATC TCT GGC ACA ACA GCT 2709
H F S S K D K I Q F V K L F F E S L F A 923
CAC TTT TCT TCC AAG GAT AAG TTG CAA GAG GTG AAA CTA TTT GAA TCT CTT GAG GCT 2769
Q G S H I D F Q I F L E I T K N I K 943
CAA GGA TCA CAT CTG GAT ATT TTT CAA ACT GTT CTG GAA AGC ATA ACC AAA AAT ATA AAA 2829
W L F K N I P T I R T V I M V N T * 961
TGG CTG GAG AAG AAT CTT CCG ACT CTG AGG ACT TGG CTA ATG GTT AAT ACT TAA 2883

ATGGTCAATAGAAAAAGTAGGCTGGGCCGGCTACGGCTGTAAATCCAGCACTTTGGAGGCTGAGAAGGGCGGA
TCACGAGGTCAAGGAGATGGAGACCATCTGGCTAACACGGTGAGACCCCGTCTCCGCTAAAAATAACAAAAATTAGCCG
GGCATGGTGGCAGGTGCCCTGTAGTCCCAGCTACTCGCAGGCTGCAGCAGGAAATGGCATAAACCCGGAGGTGGAGC
TTGCAGTGGCCGAGATTGCAACCCTGCATTCCAGCCTGGGTGACTGAGCAGAGACTCTGCTCTCAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAA

FIG. 1C.

Title: 17867: A Novel Human Aminopeptidase

Inventor(s): Kapeller-Libermann et al.

Application No. Not Assigned

Amtl. Drkt. Nr.: 35800/240749(5800-36A)

ANSWER

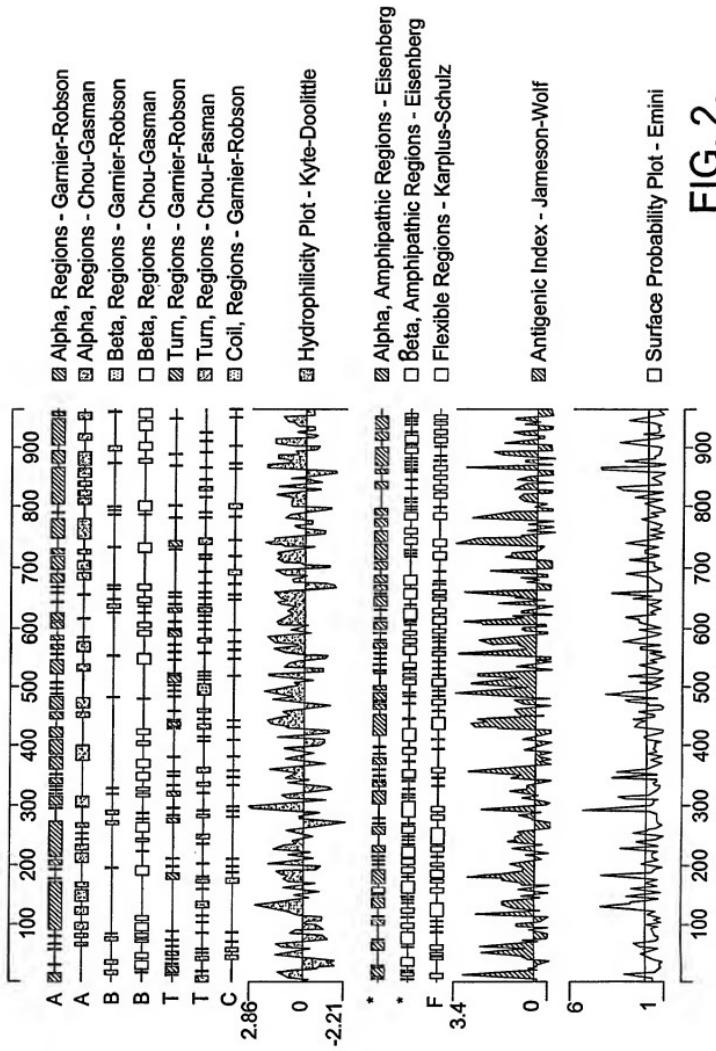


FIG. 2.

Analysis of sequence 7420 (960 aa)

no HMM hits

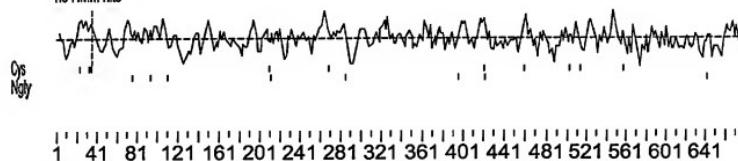


FIG. 3.

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Prosite Pattern Matches for sequence7420

>PS00001/PDC00001/ASN_GLYCOSYLATION N-glycosylation site.

Query:	85	NLTS	88
Query:	103	NATQ	106
Query:	119	NATL	122
Query:	219	NFSI	222
Query:	294	NQTH	297

FIG. 4A.

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Query: 405 NATY 408
Query: 431 NSSR 434
Query: 650 NHTL 653
Query: 714 NISD 717
Query: 879 NWTH 882

>PS00004/PDDC0004/CAMP_PHOSPHO_SITE cAMP - and cGMP-dependent protein kinase phosphorylation site.

Query: 225 RRES 228
Query: 483 KKFS 486

>PS00005/PDDC0005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 10 SHR 12
Query: 94 SEK 96
Query: 183 TYR 185
Query: 221 SIK 223
Query: 256 TVK 258
Query: 303 SLK 305
Query: 343 TYR 345
Query: 359 SDK 361
Query: 432 SSR 434
Query: 486 SYR 488
Query: 558 SLR 560
Query: 740 SDK 742
Query: 781 SGK 783
Query: 830 TSK 832
Query: 906 SSK 908
Query: 951 TLR 853

>PS0006/PDDC0006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 57 TNGE 60
Query: 87 TSLD 90
Query: 124 SEED 127
Query: 197 TDFF 200
Query: 321 SKLD 324
Query: 343 TYRE 346
Query: 357 SASD 360
Query: 407 TYPE 410
Query: 502 SCLE 505
Query: 607 SKTD 610
Query: 701 SYLE 704
Query: 738 SWSD 741
Query: 744 SWVD 747
Query: 817 SSAE 820

FIG. 4B.

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Query: 906 SSKD 909
Query: 926 SHLD 929
Query: 933 TVLE 936

>PS00007/PDOC00007/TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.

Query: 312 KYFDIYY 318
Query: 622 KFNVDNSGY 630
Query: 679 KALDMTYY 686
Query: 885 KKFDLGSY 892

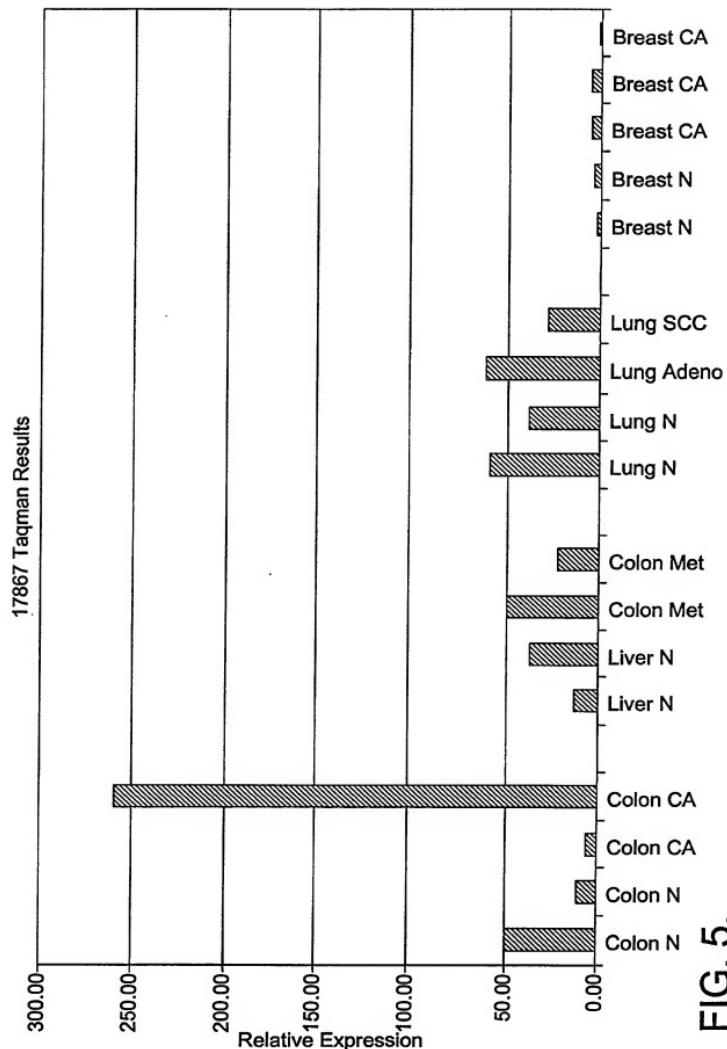
>PS0008/PDOC00008/MYRISTYL_N-myristoylation site.

Query: 281 GVKVSI 286
Query: 334 GAMENW 339
Query: 378 GNLVTH 383
Query: 512 GVCHSD 517
Query: 798 GAQTTA 803
Query: 868 QQOLAW 873

>PS00142/PDOC00129/ZINC_PROTEASE Neutral zinc metallopeptidases, zinc-binding region signature.

Query: 367 VIAHELAHW 376

FIG. 4C.

**FIG. 5.**

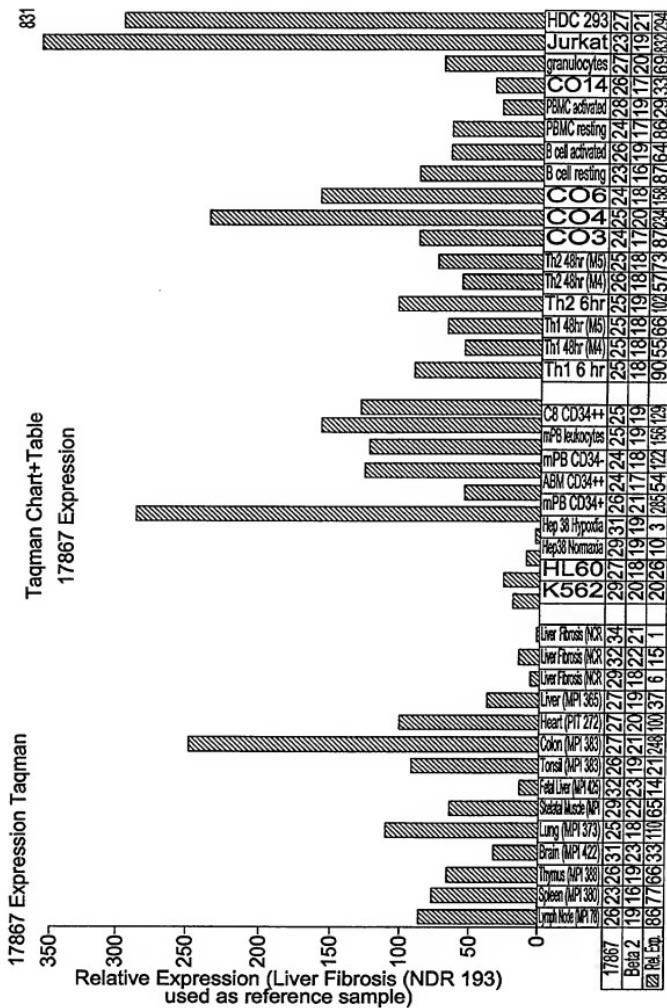


FIG. 6.